

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: RICCARDI, Carlo

(ii) TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL DEATH PATHWAYS

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

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- (C) CITY: Washington
- (D) STATE: D.C.
- (E) COUNTRY: USA
- (F) ZIP: 20001

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/403,861
- (B) FILING DATE: 11-FEB-2000

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/EP98/02490
- (B) FILING DATE: 27-APR-1998

vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: EP 97107033.9
- (B) FILING DATE: 28-APR-1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: YUN, Allen C.
- (B) REGISTRATION NUMBER: 37,971
- (C) REFERENCE/DOCKET NUMBER: RICCARDI=1

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 202-628-5197
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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 206..616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTGGCTGCTG TGGAGTTGT GACATACTAG GTGACACCCT TGGAGTCACT TCTCTTCAAC	60
TCCAGCTTAG AAGTGCCTGC CTGGCTCAGG GTCTGCACTG CAGCCTACTC CTTGCTTCAG	120
GGCCTGACTG CAACGCCAAA GCCTATCCTA TAGCGGCAGC GCCAGCAGCC ACTCAAACCA	180
GCCACAGCTC CCCGGCAACC GAACC ATG AAC ACC GAA ATG TAT CAG ACC CCC Met Asn Thr Glu Met Tyr Gln Thr Pro	232
1 5	
ATG GAG GTG GCG GTC TAT CAG CTG CAC AAT TTC TCC ACC TCC TTC TTT Met Glu Val Ala Val Tyr Gln Leu His Asn Phe Ser Thr Ser Phe Phe	280
10 15 20 25	
TCT TCT CTG CTT GGA GGG GAT GTG GTT TCC GTT AAA CTG GAT AAC AGT Ser Ser Leu Leu Gly Gly Asp Val Val Ser Val Lys Leu Asp Asn Ser	328
30 35 40	
GCC TCC GGA GCC AGT GTG GTG GCC CTA GAC AAC AAG ATT GAG CAG GCC Ala Ser Gly Ala Ser Val Val Ala Leu Asp Asn Lys Ile Glu Gln Ala	376
45 50 55	
ATG GAC CTC GTG AAG AAC CAC CTG ATG TAC GCT GTG AGA GAG GAG GTG Met Asp Leu Val Lys Asn His Leu Met Tyr Ala Val Arg Glu Glu Val	424
60 65 70	
GAG GTC CTA AAG GAG CAG ATT CGT GAG CTG CTT GAG AAG AAC TCC CAG Glu Val Leu Lys Glu Gln Ile Arg Glu Leu Leu Glu Lys Asn Ser Gln	472
75 80 85	
CTG GAG CGC GAG AAC ACC CTC CTG AAG ACG CTG GCA AGC CCC GAG CAA Leu Glu Arg Glu Asn Thr Leu Leu Lys Thr Leu Ala Ser Pro Glu Gln	520
90 95 100 105	
CTG GAA AAG TTC CAG TCC CGG CTG AGC CCT GAA GAG CCA GCA CCT GAA Leu Glu Lys Phe Gln Ser Arg Leu Ser Pro Glu Glu Pro Ala Pro Glu	568
110 115 120	
GCC CCA GAA ACC CCG GAA ACC CCG GAA GCC CCT GGT GGT TCT GCG GTG Ala Pro Glu Thr Pro Glu Thr Pro Glu Ala Pro Gly Gly Ser Ala Val	616
125 130 135	
TAAGTGGCTC TGTCTTAGG GTGGGCAGAG CCACATCTTG TTCTACCTAG TTCTTCCAG	676
TTTGTCCCCAG GGTCACTCA TGTGGAGAAC TTTACACCTA ACATAGCTGG	736
TGCCAAGAGA TGTCCCAAGG ACATGCCCAT CTGGGTCCAC TCCAGTGACA GACCCCTGAC	796
AAAGAGCAGG TCTCTGGAGA CTAAGTTGCA TGGGGCCTAG TAACACCAAG CCAGTGAGCC	856
TGTCGTGTCA CCGGGCCCTG GGGCTCCCA GGGCTGGCA ACTTAGTTAC AGCTGACCAA	916
GGAGAAAGTA GTTTGAGAT GTGATGCCAG TGTGCTCCAG AAAGTGTAAAG GGGTCTGTTT	976
TTCATTCCA TGGACATCTT CCACAGCTTC ACCTGACAAT GACTGTTCT ATGAAGAAGC	1036

CACTTGTGTT	CTAACAGAA	GCAACCTCTC	TCTTCCTCCT	CTGTCTTTTC	CAGGCAGGGG	1096
CAGAGATGGG	AGAGATTGAG	CCAAATGAGC	CTTCTGTTGG	TTAATACTGT	ATAATGCATG	1156
GCTTGTGCA	CAGCCCAGTG	TGGGGTTACA	GCTTGGGAT	GACTGCTTAT	AAAGTTCTGT	1216
TTGGTTAGTA	TTGGCATCGT	TTTCTATAT	AGCCATAATG	CGTATATATA	CCCATAGGGC	1276
TAGATCTATA	TCTTAGGGTA	GTGATGTATA	CATATACACA	TACACCTACA	TGTTGAAGGG	1336
CCTAACACCAGC	TTTGGGAGTA	CTGACTGGTC	TCTTATCTCT	TAAAGCTAAG	TTTTTGACTG	1396
TGCTAATTAA	CCAAATTGAT	CCAGTTGTC	CTTTAGATTA	AATAAGACTC	GATATGAGGG	1456
AGGGAGGGGA	AGACCAGCCT	CACAATGCAG	CCACAGATGC	CTTGCTGCTG	CAGTCCTCCC	1516
TGATCTGTCC	ACTGAAGACA	TGAAGTCCTC	TTTGAATGC	CAAACCCACC	ATTCAATTGGT	1576
GCTGACTACA	TAGAATGGGG	TTGAGAGAAG	ATCAGTTGG	ACTTCACATT	TTTGTGTTAA	1636
GTGTTAGGTT	GTGTTTTTTT	GGGTTTGT	GTGTTGTTGT	TTGTTGTTTT	TTGTTTTTG	1696
TTTCTTTT	TTAAGTTCTT	GTGGGAAAC	TTGGGGTTA	ATCAAAGGAT	GTAGTCCTGT	1756
GGTAGACCAG	AGGAGTAAC	AGTTTGATC	CTTGTTGGTG	TGGAAAATGT	ACCCAGGAAG	1816
CTTGTGTAAG	GAGGTTCTGT	GACAGTGAAC	ACTTCCACT	TTCTGACACC	TCATCCTGCT	1876
GTACGACTCC	AGGATTGGA	TTGGATT	TCAAATGTAG	CTTGAAATT	CAATAAACTT	1936
TGCTCCTTTT	TCTAAAAATA	AAAAAAAAAA	AAAAAAA			1972

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Asn	Thr	Glu	Met	Tyr	Gln	Thr	Pro	Met	Glu	Val	Ala	Val	Tyr	Gln
1				5				10						15	

Leu	His	Asn	Phe	Ser	Thr	Ser	Phe	Phe	Ser	Ser	Leu	Leu	Gly	Gly	Asp
								25					30		

Val	Val	Ser	Val	Lys	Leu	Asp	Asn	Ser	Ala	Ser	Gly	Ala	Ser	Val	Val
								35					40		45

Ala	Leu	Asp	Asn	Lys	Ile	Glu	Gln	Ala	Met	Asp	Leu	Val	Lys	Asn	His
								50					55		60

Leu	Met	Tyr	Ala	Val	Arg	Glu	Glu	Val	Glu	Val	Leu	Lys	Glu	Gln	Ile
								65					70		75

Arg	Glu	Leu	Leu	Glu	Lys	Asn	Ser	Gln	Leu	Glu	Arg	Glu	Asn	Thr	Leu
								85					90		95

Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Arg
100 105 110

Leu Ser Pro Glu Glu Pro Ala Pro Glu Ala Pro Glu Thr Pro Glu Thr
115 120 125

Pro Glu Ala Pro Gly Gly Ser Ala Val
130 135

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..20
 - (D) OTHER INFORMATION:/note= "PCR forward primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCATCTGGGT CCACTCCAGT

20

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..20
 - (D) OTHER INFORMATION:/note= "PCR reverse primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AGGACAGTG GAGTGGCACC

20

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1946 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 241..642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AATTCGGGGG CCGTGGAGTT TGTGACATAC GAGGTGACAC CCCTCGAGTC ACTTCCCTTC	60
AACTCCAGCT GGAGCGCCTG CTTGGCTTG GGTCGTTCT GCAGCCTTCG CCCCCGCTCCT	120
AGCCTCAGGG CCGGACTCCA GCGCAGAGCC CAGCCAGCG CAGCCTGCCA GCAGCCACCC	180
AGCCGCCAG CCGCCCAGCC CCGCACGAAA CCCGGCCAGA GCTTCCTAGC AGCCCGAGCC	240
ATG AAC ACC GAA ATG TAT CAG ACC CCC ATG GAG GTG GCG GTC TAC CAG Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln	288
5 10 15	
CTG CAC AAT TTC TCC ATC TCC TTC TTC TCT TCT CTG CTT GGA GGG GAT Leu His Asn Phe Ser Ile Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp	336
20 25 30	
GTG GTT TCC GTT AAG CTG GAC AAC AGT GCC TCC GGA GCC AGC GTG GTG Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val	384
35 40 45	
GCC ATA GAC AAC AAG ATC GAA CAG GCC ATG GAT CTG GTG AAG AAT CAT Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His	432
50 55 60	
CTG ATG TAT GCT GTG AGA GAG GAG GTG GAG ATC CTG AAG GAG CAG ATC Leu Met Tyr Ala Val Arg Glu Glu Val Glu Ile Leu Lys Glu Gln Ile	480
65 70 75 80	
CGA GAG CTG GTG GAG AAG AAC TCC CAG CTA GAG CGT GAG AAC ACC CTG Arg Glu Leu Val Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu	528
85 90 95	
TTG AAG ACC CTG GCA AGC CCA GAG CAG CTG GAG AAG TTC CAG TCC TGT Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Cys	576
100 105 110	
CTG AGC CCT GAA GAG CCA GCT CCC GAA TCC CCA CAA GTG CCC GAG GCC Leu Ser Pro Glu Glu Pro Ala Pro Glu Ser Pro Gln Val Pro Glu Ala	624
115 120 125	
CCT GGT GGT TCT GCG GTG TAAGTGGCTC TGTCCTCAGG GTGGGCAGAG Pro Gly Gly Ser Ala Val	672
130	
CCACTAAACT TGTTTACCT AGTTCTTCC AGTTGTTTT TGGCTCCCCA AGCATCATCT	732
CACGAGGAGA ACTTTACACC TAGCACAGCT GGTGCCAAGA GATGTCCTAA GGACATGGCC	792
ACCTGGGTCC ACTCCAGCGA CAGACCCCTG ACAAGAGCAG GTCTCTGGAG GCTGAGTTGC	852
ATGGGGCCTA GTAACACCAA GCCAGTGAGC CTCTAATGCT ACTGCGCCCT GGGGGCTCCC	912

AGGGCCTGGG CAACTTAGCT GCAACTGGCA AAGGAGAAGG GTAGTTGAG GTGTGACACC	972
AGTTTGCTCC AGAAAGTTA AGGGGTCTGT TTCTCATCTC CATGGACATC TTCAACAGCT	1032
TCACCTGACA ACGACTGTTG CTATGAAGAA GCCACTTGTG TTTTAAGCAG AGGCAACCTC	1092
TCTCTTCTCC TCTGTTCTGT GAAGGCAGGG GACACAGATG GGAGAGATTG AGCCAAGTCA	1152
GCCTTCTGTT GGTAAATATG GTATAATGCA TGGCTTGTG CACAGCCCAG TGTGGGATTA	1212
CAGCTTTGGG ATGACCGCTT ACAAAAGTTCT GTTTGGTTAG TATTGGCATA GTTTTTCTAT	1272
ATAGCCATAA ATGCGTATAT ATACCCATAG GGCTAGATCT GTATCTTAGT GTAGCGATGT	1332
ATACATATAC ACATCCACCT ACATGTTGAA GGGCCTAACCC AGCCTTGGGA GTATTGACTG	1392
GTCCTTACCC TCTTATGGCT AAGTCTTGA CTGTGTTCAT TTACCAAGTT GACCCAGTT	1452
GTCTTTAGG TTAAGTAAGA ACTCGAGAGT AAAGGCAAGG AGGGGGGCCA GCCTCTGAAT	1512
GCGGCCACGG ATGCCTTGCT GCTGCAACCC TTTCCCCAGC TGTCCACTGA AACGTGAAGT	1572
CCTGTTTGA ATGCCAAACC CACCATTACAC TGGTGCTGAC TACATAGAAT GGGTTGAGAG	1632
AAGATCAGTT TGGGCTTCAC AGTGTCAATT GAAAAAGCGT TTTTGTGTTG TTTTGAATTA	1692
TTGTGGAAAAA CTTTCAAGTG AACAGAAGGA TGGTGTCTA CTGTGGATGA GGGATGAACA	1752
AGGGGATGGC TTTGATCCAA TGGAGCCTGG GAGGTGTGCC CAGAAAGCTT GTCTGTAGCG	1812
GGTTTTGTGA GAGTGAACAC TTTCCACTTT TTGACACCTT ATCCTGATGT ATGGTTCCAG	1872
GATTGGATT TTGATTTC CAAATGTAGCT TGAAATTCA ATAAACTTTG CTCTGTTTT	1932
CTAAAAAATA AAAA	1946

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Asn	Thr	Glu	Met	Tyr	Gln	Thr	Pro	Met	Glu	Val	Ala	Val	Tyr	Gln
1				5				10						15	

Leu	His	Asn	Phe	Ser	Ile	Ser	Phe	Phe	Ser	Ser	Leu	Leu	Gly	Gly	Asp
					20			25					30		

Val	Val	Ser	Val	Lys	Leu	Asp	Asn	Ser	Ala	Ser	Gly	Ala	Ser	Val	Val
								35					40		45

Ala	Ile	Asp	Asn	Lys	Ile	Glu	Gln	Ala	Met	Asp	Leu	Val	Lys	Asn	His
					50				55				60		

Leu Met Tyr Ala Val Arg Glu Glu Val Glu Ile Leu Lys Glu Gln Ile

65 70 75 80
Arg Glu Leu Val Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu
 85 90 95
Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Cys
 100 105 110
Leu Ser Pro Glu Glu Pro Ala Pro Glu Ser Pro Gln Val Pro Glu Ala
 115 120 125
Pro Gly Gly Ser Ala Val
 130

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Leu Lys Glu Gln Ile Lys Glu Leu Ile Glu Lys Asn Ser Gln Leu Glu
1 5 10 15
Gln Glu Asn Asp Leu Leu Lys Thr Leu Ala
20 25

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu
1 5 10 15
Asn Glu Val Ala Arg Leu Lys Lys Leu Val
20 25

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Leu Glu Asn Arg Val Ala Val Leu Glu Asn Gln Asn Lys Thr Leu Ile

1 5 10 15
Glu Glu Leu Lys Ala Leu Lys Asp Leu Tyr
20 25

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Leu Glu Asn Arg Val Ala Val Leu Glu Asn Gln Asn Lys Thr Leu Ile
1 5 10 15

Glu Glu Leu Lys Ala Leu Lys Asp Leu Tyr
20 25

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn Ser Glu Leu Ala
1 5 10 15

Ser Thr Ala Asn Met Leu Arg Glu Gln Val
20 25

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Asp Leu Val Lys Asn His Leu Met Tyr Ala Val Arg Glu Glu Val
1 5 10 15

Glu Ile Leu Lys Glu Gln Ile Arg Glu Leu Val Glu Lys Asn Ser Gln
20 25 30

Leu Glu Arg Glu Asn Thr Leu Leu Lys Thr Leu Ala Ser Pro Glu Gln
35 40 45

Leu Glu Lys Phe Gln Ser Cys Leu Ser Pro Glu Glu Pro Ala Pro Glu
50 55 60

Ser Pro Gln Val Pro Glu Ala Pro Gly Gly Ser Ala Val
65 70 75

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Lys Ser Gln Trp Cys Arg Pro Val Ala Met Asp Leu Gly Val Tyr Gln
1 5 10 15

Leu Arg His Phe Ser Ile Ser Phe Leu Ser Ser Leu Leu Gly Thr Glu
20 25 30

Asn Ala Ser Val Arg Leu Asp Asn Ser Ser Ser Gly Ala Ser Val Val
35 40 45

Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Ser His
50 55 60

Leu Met Tyr Ala Val Arg Glu Glu Val Glu Val Leu Lys Glu Gln Ile
65 70 75 80

Lys Glu Leu Ile Glu Lys Asn Ser Gln Leu Glu Gln Glu Asn Asn Leu
85 90 95

Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Ala Gln Phe Gln Ala Gln
100 105 110

Leu Gln Thr Gly Ser Pro Pro Ala Thr Thr Gln Pro Gln Gly Thr Thr
115 120 125

Gln Pro Pro Ala Gln Pro Ala Ser Gln Gly Ser Gly Pro Thr Ala
130 135 140

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION:/note= "the N-terminus is modified by an acetyl group; the C-terminus is modified with a-(4-methyl-coumaryl-7-amide)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Asp Glu Val Asp

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION:/note= "the N-terminus is modified by an acetyl group; the C-terminus is modified with CH₂OC(O)-[2,6-(CF₃)₂]Ph"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Tyr Val Ala Asp